

Chapter 8 – General Conclusions

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In this thesis, I defined the concept of epidemiological interaction (EI) between two host populations and presented two approaches to estimate these EIs. The first approach (Chapter Two - Caron et al. 2009) assumed that the movements of hosts and the contacts induced by this mobility would estimate EIs. The second approach (Chapter Seven & Appendix Six) assumed that a limited quantity of potential transmission pathways exist between two host populations (e.g. direct contact, vector transmission) and that past occurrence of transmission could estimate future occurrence (disease emergence).

In the framework of this thesis, I mostly developed the first approach. Using the model of wild and domestic avian communities in a Zimbabwean wetland, I gathered regular bird count and pathogen prevalence data during two years in order to provide information about the ecology of AIV in a multi-host system and tested my assumptions on the first approach (Chapter Three, Four, Five & Six - Caron et al. 2010, Caron et al. 2011). The main outcomes of this approach were the new sanitary information provided. I suggested for the first time a persistence of AIV in an African ecosystem based on multi-species data. I provided the first occurrence of AIV in some waterfowl species and a solid three-year dataset of ornithological data. Secondly, I explored how a host community approach can help define risk season and risk species for both the epidemiological cycle (reservoir, spreader, maintenance host) and at the wildlife/domestic interface (bridge species). Chapter Three, Four & Five (Caron et al. 2010, Caron et al. 2011) explained the difficulty of estimating prevalence in multi-host systems and how this complexity could be used to provide integrated ecological and epidemiological tools improving the prevalence estimation. And finally Chapter Six presented how ecological and epidemiological data could be integrated in a risk analysis approach to estimate the risk of pathogen spread through wild birds at the wildlife/domestic interface in order to provide stakeholders with data-based decision making tools for limited-resource allocation. Articles included as appendices showed how this work was integrated in a broader

framework of research on the ecology of avian influenza viruses in African waterbirds at the regional and continental level (Appendix One, Two, Four & Five - Gaidet et al. 2007a, Gaidet et al. 2007b). In parallel, the same approach was used on wild/domestic ungulate community in the South-East Lowveld of Zimbabwe, trying to explore transmission pathways for bovine tuberculosis and other important diseases (Appendix Three - de Garine-Wichatitsky et al. 2010). This additional model provided the opportunity to explore host-pathogen interaction in a different system with a different host approach; we detected the spread of bovine tuberculosis from South Africa to Zimbabwe and established a telemetry study at the wildlife/livestock interface exploring the host approach at the population level with a social network analysis perspective (manuscript in preparation). The juxtaposition of these models highlighted the process-centred approach that I focused on instead of a host- or pathogen-centred approach: I (in collaboration with my colleagues on the second model) explored and tested the same hypotheses in the two models.

The second approach to estimate EIs was mostly developed in the Chapter Seven and Appendix Six. Here we presented a conceptual and operational framework and used the shared community of parasites between fourteen rodent species and the human species to build an interaction network. We compared it with a similar network built using trapping data to estimate host co-occurrence. We discussed the advantage and weakness of this approach and explain in which circumstances it could be used. To my mind, this method could be used as an on-going process: in a given ecosystem, ecological and epidemiological available data (e.g. through national surveillance system or NGO projects) could be integrated in a preliminary interaction network. This network could help identify the gaps in information and be re-enforced once this information is produced. This chapter had therefore two sides: a purely fundamental background rooted in the ecology of disease transmission; and an applied aspect able to help surveillance systems to identify and source the right information and

provide health managers with control options for emerging diseases. In the near future, the two models developed in this thesis (the avian and ungulate models) will provide the data needed to validate this approach empirically. Wild birds sampled have been or will be tested for Newcastle disease, West Nile Virus and Avian Malaria. In addition, domestic and wild ungulates have been tested for bovine tuberculosis, Foot-and-Mouth Disease, Rift Valley Fever, Brucellosis, the most common tick-borne diseases (theileriosis, babesiosis, anaplasmosis), Lumpy Skin Diseases and faecal macroparasites.

From a critical point of view, if this thesis has developed new analytical tools at the interface of different scientific fields (epidemiology and ecology), it was confronted to a level of complexity (multi-host, multi-pathogen systems) not fully integrated in the products. This thesis should be seen as opening new avenues for future research rather than delivering a final output. Furthermore, the level of analysis of this work is embedded in lower levels of host-pathogen interaction, at the individual level and at the molecular level (e.g. immunology, molecular epidemiology) which should be controlled for or at least acknowledge when analysing eco-epidemiological data with the approaches presented here.

The complexity of multi-host systems prevents a clear-cut analysis of host and pathogen interaction at the host community level. The range of possible interactions between hosts and between pathogens becomes quickly impossible to track. However leaving aside the host community level is detrimental to epidemiological studies. Haydon et al. (2002) present different configurations of a multi-host reservoir. Surveillance or control management options missing an important host in a multi-host reservoir will fail. Similarly, Telfer et al. (2010) recently demonstrated how interactions between pathogens in a host population can bias the results of single-pathogen studies. Both these studies are important because of the two major shifts in wildlife/domestic epidemiology they induce: 1) most data produced to date have to be interpreted with caution as underlying interactions between parasites or influence by

unknown hosts can interfere with the direct host-parasite interaction observed; 2) analytical tools to estimate real host-pathogen interactions based on limited ecological and epidemiological information are not yet available or not yet integrated between the various fields of ecology and veterinary sciences. This is important to realise as our focus concerning emerging infectious diseases is now turning towards epidemiological systems embedded in this complexity at the wildlife/domestic/human interface (Cleaveland et al. 2001, Taylor et al. 2001). Most emergence events will occur in multi-host systems hot spots (Jones et al. 2008). This could be seen as a rather pessimistic perspective for animal and human health. I believe it is not. Efforts will be necessary to produce the interdisciplinary mixing, needed between researchers but also for individual profiles through proper academic careers. The research community already has tools available to analyse this complexity which needs to be integrated across different thematic fields. I have tried to show in my thesis how the integration of tools borrowed from community ecology and epidemiology bring more information than a separated analysis by each field. As presented in the last chapter of this thesis, evolutionary biology feeding molecular epidemiology can also help in identifying the direction of transmission pathways. However, the technological power necessary to have an exhaustive study at the ecosystem level of hosts and parasites species is not yet to hand.

Today, epidemiologists and health ecologists face the dilemma faced by ecologists when they apprehended the complexity of the study of organisms' interactions at the community level: the impossibility of taking into account the full spectrum of host-pathogen interactions at the community level with the tools available. However, patterns and general rules can still be extracted from the complexity and I hope this thesis can provide concepts and frameworks to reach this objective.

However, in a final futuristic comment, I would state that I think that the ecology of disease transmission or the study of epidemiology at the host-pathogen community level will

soon have a net advantage on community ecology investigating ecological interactions between non-parasite organisms. When a host-pathogen interaction occurs, it leaves a “trace” in the host and/or in the pathogen. This trace can be: 1) the presence of the pathogen or of products of the immune system responding to the presence (or past presence) of the pathogen; 2) it can also be a change in the genome of the host or the pathogen (induced mutation, evolutionary response to the interaction). These traces of host-pathogen interaction can be used at the community level as a history of epidemiological interactions. As an example, the development of non-invasive techniques to detect the presence of pathogens in faeces is providing professionals with an amount of available data with low cost of sampling (no need of physical capture for this type of wildlife sampling). The recent development of a broad spectrum genetic material detection machine – broad range acid nucleic sequencer - (Gupta et al. 2009, Holmes and Grenfell 2009) makes clear the point that it is already possible to extract from any substrate (e.g. tissue, faeces) the entire community of acid nucleic sequences. This broad spectrum detection refers to known and unknown acid nucleic sequences. So far, we lack the power needed to analyse and segregate such a huge amount of data. In a few years, we will have at hand those analytical tools.

In conclusion, I believe this thesis explored ways to further development in the ecology of disease transmission. By addressing questions at the transmission process-level, it explores what could be the general properties and/or rules governing disease transmission, independently of the pathogen at stake. There may be none, but if they exist, they could change some current practices in disease management.

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